HOST- MICROBIOME INTERACTIONS

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Book of abstracts

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Fructooligosaccharide-driven metabolism of a probiotic consortium modulates hepatocyte lipid accumulation in an *in vitro* microbiota-liver interaction model

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Metabolic-dysfunction-associated fatty liver disease (MAFLD) is a metabolic disorder in which the gut-liver axis plays a central role. Microbial-derived metabolites generated from dietary substrates are key mediators linking gut microbiota activity to host metabolic regulation. Specifically, fructooligosaccharides (FOS) can modulate microbial metabolism and functional outputs.

We investigated the impact of FOS-driven microbial metabolism on hepatic lipid accumulation using a defined *in vitro* human gut microbiota model. A probiotic consortium composed of *Lactiplantibacillus plantarum*, *Lactobacillus acidophilus*, and *Limosilactobacillus reuteri* was evaluated alone and in combination with a reconstructed minimal human gut microbiota core (*Clostridum symbiosum*, *Flavonifractor plautii*, *Bacteroides cellulosilyticus*, and *Escherichia coli*). Bacterial growth, strain-level dynamics, and expression of genes involved in FOS utilization were assessed. Microbial metabolites were characterized by GC-MS and tested on HepG2 cells in a palmitic acid-induced steatosis model.

All strains grew on FOS, with strain-dependent efficiency. The probiotic consortium and the overall microbial community were shaped by substrate utilization, with *L. plantarum* and *L. reuteri* dominating in both contexts. Genes involved in FOS metabolism were identified in all probiotic strains, showing differences in gene organization, and expression across different experimental conditions.

FOS fermentation resulted in the production of short-chain fatty acids and organic acids. HepG2 cells pre-treated with metabolites derived from the probiotic consortium and the reconstructed community showed reduced intracellular lipid accumulation under steatotic conditions, associated with decreased *cd36* lipid transporter gene expression.

These findings highlight the role of microbial context in shaping metabolic outputs and support the contribution of microbial interactions to the regulation of host lipid metabolism in a liver cell model.

How are microbiomes transmitted across animals? An integrative approach to quantify the ecological factors driving microbiome transfer using guppies.

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Microorganisms play an essential role in animal health, yet the mechanisms governing their colonization and transmission are poorly understood. Here, we investigated microbiome transmission using guppies (*Poecilia reticulata*), a established model in animal behavioral ecology. The aquatic environment offers the advantage to disentangle the environment from the host-driven processes of microbiome dispersal. We generated two cohorts of guppies with distinct microbial profiles and placed them in cohabitation with and without contact. Using an integrative framework combining genomics (16S rRNA, metagenomics), behavioral tracking, fluorescence microscopy, and ecological modelling we characterized microbiome dynamics across four host compartments (skin gills, gut, gonads). Our results reveal distinct transmission pathways for external versus internal microbiomes, along with pronounced sex- and microbial-specific differences. Understanding how microbiomes move between hosts, and how these processes differ across organs, is essential for elucidating microbiome function and holds great potential for optimizing microbiome-based interventions across diverse animal taxa, including humans.

Talking roots: a genotype-specific interactive dialogue between endophytic bacteria and wild and domesticated rice revealed by multi-omics

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Plant-microbe interactions are crucial for plant health and productivity, and root exudates play a central role in shaping these associations. Here, we investigated the bidirectional transcriptional and hormonal dialogue between rice and two endophytic plant growth-promoting bacteria using an integrated multi-omics approach.

We exposed *Enterobacter asburiae* RCA24 and *Kosakonia sacchari* RCA25 to root exudates from three rice genotypes: two cultivated varieties (*Oryza sativa* cv. Baldo and Vialone Nano) and the wild ancestor *Oryza rufipogon*. Bacterial RNA-seq revealed genotype-by-genotype interactions: *E. asburiae* RCA24 was able to distinguish between *O. sativa* varieties, and *K. sacchari* RCA25 responded more strongly to *O. rufipogon* exudates. Functional annotation highlighted differential expression of genes involved in central metabolism, stress response, and signal transduction among the cultivated and wild rice genotypes, suggesting that domestication has reduced the stimulatory capacity of rice exudates on beneficial microbes.

Hormonomic profiling of root exudates revealed genotype-specific phytohormone signatures. Gibberellins showed strong differentiation (PERMANOVA R^2=0.53, p=0.006), with GA_9 characterizing Baldo (956 pmol/L) and GA_{51} dominating *O. rufipogon* (577 pmol/L). Auxin profiles exhibited moderate genotypic variation (R^2=0.39, p=0.034).

To assess reciprocal effects, we also analyzed the rice transcriptome following bacterial colonization. The analysis revealed that bacterial colonization triggered tissue- and genotype-dependent responses. For *E. asburiae* RCA24, 3,813 differentially expressed genes were observed in Baldo stems, while for *O. rufipogon,* limited transcriptional responses were recorded.

Overall, these findings highlight the reciprocal and genotype-specific transcriptional crosstalk between rice and endophytic bacteria, demonstrating that *O. rufipogon* may be a reservoir of traits that could be exploited to optimize rice-microbe interactions that promote plant growth for sustainable agriculture.

Phylogenetically stratified GWAS reveals insights into *Escherichia coli* specific virulence factors in adults and neonates

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Escherichia coli is a highly diverse bacterial species capable of occupying a wide range of ecological niches, from harmless gut commensalism to severe extraintestinal infections. Identifying genetic determinants that underlie adaptation to specific host and environmental contexts remains challenging due to extensive horizontal gene transfer and strong phylogenetic structure. In this study, we performed a genome-wide association study (GWAS) on gene presence–absence across a large collection of *E. coli* genomes isolated from adult and neonatal bloodstream infections, urinary tract infections, healthy gut, hospital settings, and non-clinical environmental sources. By explicitly accounting for population structure, we identified lineage-independent, source-associated genetic signatures while minimizing confounding by vertically inherited genes.

Bloodstream and urinary isolates were significantly enriched in genes involved in metal acquisition (iron and manganese), adhesion, biofilm formation, and stress responses, highlighting shared adaptations for survival in hostile host environments. Neonatal bloodstream isolates showed a strong association with the yersiniabactin iron-scavenging system, whereas adult bloodstream isolates were enriched in acid resistance genes suggesting age-specific infection routes and virulence strategies. Urinary isolates exhibited marked metabolic flexibility, with enrichment of genes related to metal acquisition, sugar uptake, and secretion systems, consistent with adaptation to the nutrient-limited urinary tract.

Together, these findings demonstrate that *E. coli* adapts to distinct ecological and clinical niches through the acquisition and maintenance of functionally relevant genes independent of phylogenetic background. Source-specific genetic traits identified here provide valuable insights into *E. coli* pathogenesis, highlight age-dependent virulence mechanisms, and offer potential biomarkers for diagnostics, surveillance, and targeted intervention strategies, particularly in vulnerable populations such as neonates and hospitalized patients.